APRROYEC	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAH	

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54 GTG	108 ACC T	162 GAG E	216 GAT D	270 ATT I	324 CTT L	378 GCC A
CTG	AGC	AAT N	AAG K	GAG	AAA K	GGT
999	TTC	AAA K	GAT D		GGA	
45 TGC	99 060 0	153 CTC L	207 GCA A	261 AAA K	315 AAA K	369 AAC N
0 0 0 0	AGC	TTC	TAT	GCA	AAA K	TGG
သဗ	ATG M	GTC	ATT	AAT	GTG V	ATC
36 950 0	90 ACT P	144 CGA R	198 CCA P	252 TCT S	306 GAT D	360 TAT Y
TCA GTC	299	GAG TAC E Y	ATT I	TGG W	CAA	GGA
	TCC	GAG	GAT	CGC	AAA K	AAA K
27 TTG	81 GAC	135 CTG L		243 CCA P		351 TAT Y
TCC	CAG	TCC		GTA V		
			CCA			
18 GCT	72	126 CCC P	180 TCT S	234 GTT V	288 TTA L	342 TTG L
- <del> </del>	99	GCG A	ATA		CG.	AAT N
TT	CAG	GCC	TAT Y		GAC	GCG A
AGG	63 TGG	117 CGC R	171 CAA Q	225 CAC H	279 4AG K	333 GTT V
AAG	63 GCT CTG TGG	GAG	GGA	LTT 7	r ACA 7 T	333 TAT GTT GCG Y V A
9 5' NNC AAG AGG T'IN	GCT	117 GAG GAG CGC E E R	AAA GGA K G	GTG 1	GCT	CGC R
5					•	

### FIGURE1A

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•						
432 TGT C	486 AGA R	540 GGG G	594 AAT N	.648 ACT T	702 TTT F	756 AGC S
		GAA				
9 9	TGT C	GAC	GCA	GAA E	AAT N	ATT
423 ACT T	477 GTA V	531 ATT I	585 GAT D	639 TTA L	693 GAA E	747 ATT I
CAT	AAG	ATG M	CCT	TAC	CCA	GAT
AAA K	AGC	GCT	GAT D	0 0 0	AAA K	ATT
414 GAT D	468 GGA G	522 TTG	576 GAT D	630 CCT P	684 GGA G	738 GCC A
AAT N	ATT I	ATA I	GTG	AAA K	GAT	TTT
CAC H	GAA	ე ე	AAT N	CTG	CCT	GAC
405 GGG G	459 TGT C	513 CTA L	567 ATT I	621 CGG R	675 GTT V	729 AAG K
		GTT V	GCC	AAA K	AAG K	GAT D
	GAT D	AAA	ATT I	GTC	TAT	<b>AAA</b>
396 GAA E		504 GTG V	558 GTC V	612 GAT D	666 AGG R	720 TTT F
TGG W	CCA	ය වි	AAA	AAT	AGA	GAA
ACT	GAC	ATT (	TGG W	ATC	TTT F	GCA
387 CAG Q	441 AAT N	495 ATA I	549 GAC D	.603 GAT D	657 TGG W	711 AAT N
CCT	GAC	GAA E	ACC	AAT N	GAC D	TTT
ATC	GGT	495 GGT GAA ATA A G E I ]	GAA	TAT Y	GTG V	GCG

### FIGURE 1B

APPROVED	0.G. I	FIG.
ΒŶ	CLASS	SUBCLASS
DRAFTSMAH		*

2					1	
810	ATC I	864 GCT A	918 GTA V	972 TCT	1026   AAA	1080
	GGA G	GAT D	ACA T	T.C	AGT	1080 AAA GTA AAT
*	AAA K	CCT	D D D	GAT T	AGA	AAA
	GGA G	855 GAT D	909 GCC A	963 TAA TGA	1008 TGT TCA TCT GGA TGT ATT	1071 CAT CTA ACT
	AAT N	TGT	S TCT	TAA	TGT	CTA
	ACG T	AAG K	GAA E	AAC	GGA	CAT
792	AAA K	846 TTC	900 TGT	954 AAA K	1008 TCT	1062 AGA ACT
	AAG K	CCC	CCC	CAG	TCA	AGA
• .	ACT T	AGC S	CCA (	CAC H	TGT	TGT
783	GTG V	837 GAG E	891 CCA P	945 CAT H	999 TCG	1053 FAA ATT
	TTA L	TCT	TTA L	TTC	ACA	G '
	GCA	TIG	GCT.	T ™	<u>-</u>	CIT
774		828 ACT T	882 GAT ( D	936 AAG 7 K	990 ATT (	
	TGG W	Ą	CTC \	GAT D	AT	CA 1
	E 3	A E	<u>ن</u> ک	<u>Б</u>	<u>.</u>	Ē
	CAT	AAT	ATT	GTG	GCT	TTT
765	GAC	819 ATG M	873 GCC A	927 GAC D	981 CAA	1035
	CAT H	TGC	AGA R	ACA	981 GGA ATA CAA GCT GAT	1035 AGT AGT AGC TTT TCA AAG
	ACT CAT GAC CAT T	AGT TGC ATG AAT AG S C M N T	873 GCC AGA GCC AT A R A I	927 CCA ACA GAC GTG G P T D V D	GGA	AGT

# FIGURE 1C

APPROVED O.G. FIG.

BY CLASS SUBCLASS

DRAFTSMAH

1089 1098 1107 1116 1125 1134 TCT GCT GTG ACT AAT CCA ATA TAC TCA GAA TGT TAT CCA TCT AAA GCA TTT TTC 1089

1188 ATA TCT CAA CTA AGA TAA CTT TTA GCA CAT GCT TAA ATA TCA AAG CAG TTG TCA 1179 1170 1161 1152 1143

1197 1206 1215 1224 1233 1242 TTT GGA AGT CAC TTG TGA ATA GAT GTG CAA GGG GAG CAC ATA TTG GAT GTA TAT

GTT ACC ATA TGT TAG GAA ATA AAA TTA TTT TGC TG 3'

## FIGURE 1D

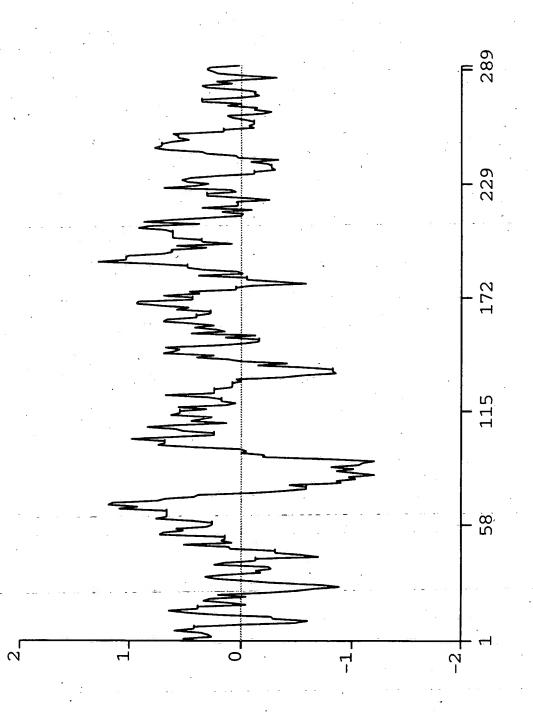
APPROVED O.G. FIG. CLASS SUBCLASS EY. DRAFTSMAH

HPYP	HPYP	HPYP	HPYP
g727225	g727225	g727225	g727225
g585322	g585322	g585322	g585322
g4199	g4199	g4199	a4199
1 MSGFSTEERAAPFSLEYRVFLKNEKGQYISPFHDIPIYAD 1	41 KD VFHMVVEVPRWSNAKMEIATKDPLNPIKODVKKGKL 1	RYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDND  1NIFPYKGYIWNYGTLPQTWEDPHEKDKSTNCFGDND  79 RYVANLFPYKGYIWNYGAIPQTWEDPGHNDKHTGCCGDND  79 RYVANLFPYKGYIWNYGAFPQTWEDPNVSHPETKAVGDND	119 PIDVCEIGSKVCARGEIIGVKVLGILAMIDEGETDWKVIA 37 PIDVCEIGSKILSCGEVIHVKILGILALIDEGETDWKLIA 119 PIDVCEIGSKVCARGEIIRVKVLGILAMIDEGETDWKVIA 119 PIDVLEIGETIAYTGOVKOVKALGIMALLDEGETDWKVIA

OSKISTO LICESS

INV DD PDAANYND INDVKRLKPGYLEATVDWFRRYKVPDG HPYPINAND PEASKFHD IDDVKKFKPGYLEATLNWFRLYKVP G727225 INVED PDAANYND INDVKRLKPGYLEATVDWFRRYKVPDG 9585322 ID INDPLAPKLND IEDVEKYFPGLLRATNEWFRIYKIPDG 94199	FNAEFKDK DFAIDIIKSTHDHWKALVT-KKTNG HPVP 9727225 FNAEFKDK NFAIDIIESTHDYWRALVT-KKTDG 9585322 FSGEAKNK KYALDIIKETHDSWKQLIAGKSSDS 94199	TTLSESPFKCDPDAARAIVDALPPC-ESACTV HPYP  TTVSESPFQCDPDAAKAIVDALPPPC-ESACTI 9585322 VTLPDTPTYSKAASDAIPPASLKADAPI 94199	F H H Q K N         F H H Q K N         F H H Q K N         G4199
159 I N V D D P D A A N Y 7 I N A N D P E A S K F 159 I N V E D P D A A N Y 159 I D I N D P L A P K L	199 KPENEFAFNA I 114 199 KPENQFAFSGE	238 K G I S C M N T T L S 114 238 K G I S C M N T T V S 239 K G I D L T N V T L P	HHH

CEBOLT TACET

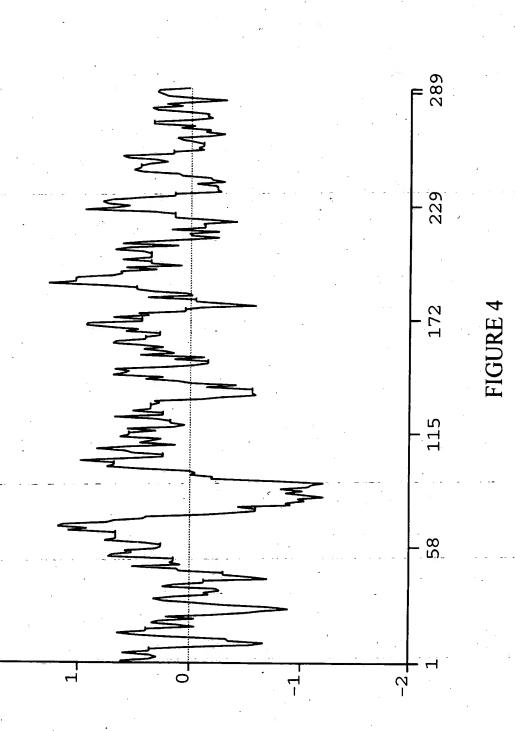


IGURE 3

APPROVED	0.G. F	FIG.	
BY	CLASS	SUBCLASS	
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APPROVED	0.G.	FIG.
BY	CLASS	SUBCLASS
DRAFTSMAH		

Library	Lib Description	Abun	Pct Abun
AML BNOT 01	AML blast cells, blast crisis, 58 F	, — — — — — — — — — — — — — — — — — — —	0.1049
THYRNOT01	thyroid, 64 F	<b>1</b> ~	0.0683
TBLYNOTO1	T-B lymphoblast cell line, leukemia	<b>5</b>	0.0651
COLNTUTO3	colon tumor, 62 M, match to COLANOT16	<b>5</b>	0.0543
U937NOT01	U937 monocyte cell line, 37 M	1-1	0.0495
TESTINOT01	testis, 37 M	I —	0.0469
HINTZAGT01	hMT-2 cell line, post-mitotic neurons	7	0.0380
PROSTUTO3	prostate tumor, 67 M, match to PROSNOT05	<b>-</b> -	0.0351
LVENNOTO3	heart, left ventricle, 31 M	ī	0.0336
BRSTNOT03	breast, 54 F, match to BRSTTUTO2	12	0.0293
PANCNOT07	pancreas, fetal M	i	0.0286
<b>BEPINON01</b>	bronchial epithelium, primary cell line, 54 M, NORM	<b>ا</b>	0.0273
PANCTUTO1	pancreatic tumor, 65 F, match to PANCNOT08	۱~	0.0257
MENITUTO 3	brain tumor, benign meningioma, 35 F	1-	0.0249
TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR		0.0228
COLNTUTO2	colon tumor, 75 M, match to COLANOT01	<del>ا</del> ا	0.0220
SYNORAB01	synovium, hip, rheumatoid, 68 F	I = 4	0.0194
LUNGNOT04	lung, 2 M		0.0182
SYNORAT04	synovium, wrist, rheumatoid, 62 F		0.0173
NGANMOT01	ganglioneuroma, 9 M	<b>٦</b>	0.0155
BRSTNOTUS	breast, 58 F, match to BRSTTUT03	<b>-4</b>	0.0154

#### IGURE 5